



#4

SEQUENCE LISTING

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<120> NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS AND METHODS
OF SCREENING FOR COLORECTAL CANCER MODULATORS

<130> A-69796/DJB/JJD

<140> US 09/733,757

<141> 2000-12-08

<160> 3

<170> PatentIn version 3.0

<210> 1

<211> 2103

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(2103)

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Met Leu Ser Ser Thr Asp Phe Thr Phe Ala Ser Trp Glu Leu
1 5 10

gtg gtc cgc gtt gac cat ccc aat gaa gag cag cag aaa gac gtc aca 159
Val Val Arg Val Asp His Pro Asn Glu Glu Gln Gln Lys Asp Val Thr
15 20 25 30

ctg aga gta tct gga gac ctt cac gtt gga gga gtg atg ctc aag tta 207
Leu Arg Val Ser Gly Asp Leu His Val Gly Gly Val Met Leu Lys Leu
35 40 45

gta gaa cag atc aat ata tcc caa gac tgg tca gac ttt gct ctt tgg 255
Val Glu Gln Ile Asn Ile Ser Gln Asp Trp Ser Asp Phe Ala Leu Trp
50 55 60

tgg gaa cag aag cat tgc tgg ctt ctg aaa acc cac tgg acc ctg gac 303
Trp Glu Gln Lys His Cys Trp Leu Leu Lys Thr His Trp Thr Leu Asp
65 70 75

aaa tat ggg gtc cag gca gat gca aag ctt ctc ttc acc cct cag cat 351
Lys Tyr Gly Val Gln Ala Asp Ala Lys Leu Leu Phe Thr Pro Gln His
80 85 90

aaa atg ctg cgc ctt cgt ctg ccg aat ttg aag atg gtg agg ttg cga 399
Lys Met Leu Arg Leu Arg Leu Pro Asn Leu Lys Met Val Arg Leu Arg
95 100 105 110

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gtc agc ttc tca gct gtg gtt ttt aaa gct gtc agt gat atc tgc aaa	447
Val Ser Phe Ser Ala Val Val Phe Lys Ala Val Ser Asp Ile Cys Lys	
115 120 125	
atc ctg aat att aga aga tca gaa gag ctt tcc ttg tta aag ccg tct	495
Ile Leu Asn Ile Arg Arg Ser Glu Glu Leu Ser Leu Leu Lys Pro Ser	
130 135 140	
ggc gac tat ttt aag aag aag aag aaa aaa gac aaa aat aat aag gaa	543
Gly Asp Tyr Phe Lys Lys Lys Lys Lys Lys Asp Lys Asn Asn Lys Glu	
145 150 155	
ccc ata att gaa gat att cta aac ctg gag agt tct cca aca gct tca	591
Pro Ile Ile Glu Asp Ile Leu Asn Leu Glu Ser Ser Pro Thr Ala Ser	
160 165 170	
ggc tca tca gta agt cct ggc tta tac agt aaa acc atg acc cct ata	639
Gly Ser Ser Val Ser Pro Gly Leu Tyr Ser Lys Thr Met Thr Pro Ile	
175 180 185 190	
tat gac ccc atc aat gga aca cca gca tca tcc acc atg act tgg ttc	687
Tyr Asp Pro Ile Asn Gly Thr Pro Ala Ser Ser Thr Met Thr Trp Phe	
195 200 205	
agt gac agc cct ttg acg gaa caa aac tgc agc atc ctc gca ttc agc	735
Ser Asp Ser Pro Leu Thr Glu Gln Asn Cys Ser Ile Leu Ala Phe Ser	
210 215 220	
caa ccc ccc cag tcc cca gaa gca ctt gcg gat atg tac cag cct cgg	783
Gln Pro Pro Gln Ser Pro Glu Ala Leu Ala Asp Met Tyr Gln Pro Arg	
225 230 235	
tct ctg gtt gat aaa gcc aag ctc aat gca ggc tgg cta gac tcc tca	831
Ser Leu Val Asp Lys Ala Lys Leu Asn Ala Gly Trp Leu Asp Ser Ser	
240 245 250	
cgc tcc ctt atg gaa caa ggc atc caa gag gat gag cag ctg ctc tta	879
Arg Ser Leu Met Glu Gln Gly Ile Gln Glu Asp Glu Gln Leu Leu Leu	
255 260 265 270	
cga ttt aaa tat tat tct ttc ttc gac ttg aat cct aaa tat gat gct	927
Arg Phe Lys Tyr Tyr Ser Phe Phe Asp Leu Asn Pro Lys Tyr Asp Ala	
275 280 285	
gtc cga ata aac caa ctc tat gag caa gcc agg tgg gcc att ctc tta	975
Val Arg Ile Asn Gln Leu Tyr Glu Gln Ala Arg Trp Ala Ile Leu Leu	
290 295 300	
gaa gaa att gat tgc aca gag gaa gaa atg ttg atc ttt gca gct cta	1023
Glu Glu Ile Asp Cys Thr Glu Glu Glu Met Leu Ile Phe Ala Ala Leu	
305 310 315	
cag tac cac att agc aaa ctg tcg ttg tct gct gaa aca cag gat ttt	1071
Gln Tyr His Ile Ser Lys Leu Ser Leu Ser Ala Glu Thr Gln Asp Phe	
320 325 330	
gca ggc gag tcc gag gtt gat gaa ata gaa gcg gcg ctt tct aat ttg	1119
Ala Gly Glu Ser Glu Val Asp Glu Ile Glu Ala Ala Leu Ser Asn Leu	

335	340	345	350	
gaa gta acc cta gaa ggt gga aaa gcg gac agc ctt ttg gag gac att Glu Val Thr Leu Glu Gly Gly Lys Ala Asp Ser Leu Leu Glu Asp Ile 355 360 365				1167
act gat atc cct aaa ctt gca gat aat ctc aaa tta ttt agg ccc aag Thr Asp Ile Pro Lys Leu Ala Asp Asn Leu Lys Leu Phe Arg Pro Lys 370 375 380				1215
aag tta cta cca aaa gct ttc aaa caa tat tgg ttt atc ttt aaa gac Lys Leu Leu Pro Lys Ala Phe Lys Gln Tyr Trp Phe Ile Phe Lys Asp 385 390 395				1263
aca tcc ata gca tac ttt aaa aat aag gaa ctt gaa caa gga gaa cca Thr Ser Ile Ala Tyr Phe Lys Asn Lys Glu Leu Glu Gln Gly Glu Pro 400 405 410				1311
cta gaa aaa cta aat ctt aga ggc tgc gaa gtt gtg ccc gat gta aat Leu Glu Lys Leu Asn Leu Arg Gly Cys Glu Val Val Pro Asp Val Asn 415 420 425 430				1359
gta gca gga aga aaa ttt gga atc aag tta cta atc cct gtt gcc gat Val Ala Gly Arg Lys Phe Gly Ile Lys Leu Leu Ile Pro Val Ala Asp 435 440 445				1407
ggt atg aat gaa atg tat ttg aga tgt gac cat gag aat caa tac gcc Gly Met Asn Glu Met Tyr Leu Arg Cys Asp His Glu Asn Gln Tyr Ala 450 455 460				1455
caa tgg atg gct gcc tgc atg ttg gca tcg aag ggc aaa acc atg gca Gln Trp Met Ala Ala Cys Met Leu Ala Ser Lys Gly Lys Thr Met Ala 465 470 475				1503
gac agc tcc tac cag cca gag gtc ctc aac atc ctt tca ttt ctg agg Asp Ser Ser Tyr Gln Pro Glu Val Leu Asn Ile Leu Ser Phe Leu Arg 480 485 490				1551
atg aaa aac agg aac tct gca tct cag gtg gct tcc agt ctc gaa aac Met Lys Asn Arg Asn Ser Ala Ser Gln Val Ala Ser Ser Leu Glu Asn 495 500 505 510				1599
atg gat atg aac cca gaa tgt ttt gtg tca cca cgg tgt gca aag aaa Met Asp Met Asn Pro Glu Cys Phe Val Ser Pro Arg Cys Ala Lys Lys 515 520 525				1647
cac aaa tcc aaa cag ctg gcc gcc cgg atc ctg gag gcg cac cag aac His Lys Ser Lys Gln Leu Ala Ala Arg Ile Leu Glu Ala His Gln Asn 530 535 540				1695
gtg gcc cag atg ccc ctg gtc gaa gcc aag ctg cgg ttc atc cag gcg Val Ala Gln Met Pro Leu Val Glu Ala Lys Leu Arg Phe Ile Gln Ala 545 550 555				1743
tgg cag tca ctg cct gag ttt ggc ctc acc tac tac ctt gtc aga ttt Trp Gln Ser Leu Pro Glu Phe Gly Leu Thr Tyr Tyr Leu Val Arg Phe 560 565 570				1791

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Leu Arg Leu Arg Leu Pro Asn Leu Lys Met Val Arg Leu Arg Val Ser
100 105 110

Phe Ser Ala Val Val Phe Lys Ala Val Ser Asp Ile Cys Lys Ile Leu
115 120 125

Asn Ile Arg Arg Ser Glu Glu Leu Ser Leu Leu Lys Pro Ser Gly Asp
130 135 140

Tyr Phe Lys Lys Lys Lys Lys Lys Asp Lys Asn Asn Lys Glu Pro Ile
145 150 155 160

Ile Glu Asp Ile Leu Asn Leu Glu Ser Ser Pro Thr Ala Ser Gly Ser
165 170 175

Ser Val Ser Pro Gly Leu Tyr Ser Lys Thr Met Thr Pro Ile Tyr Asp
180 185 190

Pro Ile Asn Gly Thr Pro Ala Ser Ser Thr Met Thr Trp Phe Ser Asp
195 200 205

Ser Pro Leu Thr Glu Gln Asn Cys Ser Ile Leu Ala Phe Ser Gln Pro
210 215 220

Pro Gln Ser Pro Glu Ala Leu Ala Asp Met Tyr Gln Pro Arg Ser Leu
225 230 235 240

Val Asp Lys Ala Lys Leu Asn Ala Gly Trp Leu Asp Ser Ser Arg Ser
245 250 255

Leu Met Glu Gln Gly Ile Gln Glu Asp Glu Gln Leu Leu Leu Arg Phe
260 265 270

Lys Tyr Tyr Ser Phe Phe Asp Leu Asn Pro Lys Tyr Asp Ala Val Arg
275 280 285

Ile Asn Gln Leu Tyr Glu Gln Ala Arg Trp Ala Ile Leu Leu Glu Glu
290 295 300

Ile Asp Cys Thr Glu Glu Glu Met Leu Ile Phe Ala Ala Leu Gln Tyr
305 310 315 320

His Ile Ser Lys Leu Ser Leu Ser Ala Glu Thr Gln Asp Phe Ala Gly
325 330 335

Glu Ser Glu Val Asp Glu Ile Glu Ala Ala Leu Ser Asn Leu Glu Val
340 345 350

Thr Leu Glu Gly Gly Lys Ala Asp Ser Leu Leu Glu Asp Ile Thr Asp
355 360 365

Ile Pro Lys Leu Ala Asp Asn Leu Lys Leu Phe Arg Pro Lys Lys Leu
370 375 380

Leu Pro Lys Ala Phe Lys Gln Tyr Trp Phe Ile Phe Lys Asp Thr Ser
385 390 395 400

Ile Ala Tyr Phe Lys Asn Lys Glu Leu Glu Gln Gly Glu Pro Leu Glu
405 410 415

Lys Leu Asn Leu Arg Gly Cys Glu Val Val Pro Asp Val Asn Val Ala
420 425 430

Gly Arg Lys Phe Gly Ile Lys Leu Leu Ile Pro Val Ala Asp Gly Met
435 440 445

Asn Glu Met Tyr Leu Arg Cys Asp His Glu Asn Gln Tyr Ala Gln Trp
450 455 460

Met Ala Ala Cys Met Leu Ala Ser Lys Gly Lys Thr Met Ala Asp Ser
465 470 475 480

Ser Tyr Gln Pro Glu Val Leu Asn Ile Leu Ser Phe Leu Arg Met Lys
485 490 495

Asn Arg Asn Ser Ala Ser Gln Val Ala Ser Ser Leu Glu Asn Met Asp
500 505 510

Met Asn Pro Glu Cys Phe Val Ser Pro Arg Cys Ala Lys Lys His Lys
515 520 525

Ser Lys Gln Leu Ala Ala Arg Ile Leu Glu Ala His Gln Asn Val Ala
530 535 540

Gln Met Pro Leu Val Glu Ala Lys Leu Arg Phe Ile Gln Ala Trp Gln
545 550 555 560

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Ser Leu Pro Glu Phe Gly Leu Thr Tyr Tyr Leu Val Arg Phe Lys Gly
 565 570 575

Ser Lys Lys Asp Asp Ile Leu Gly Val Ser Tyr Asn Arg Leu Ile Lys
 580 585 590

Ile Asp Ala Ala Thr Gly Ile Pro Val Thr Thr Trp Arg Phe Thr Asn
 595 600 605

Ile Lys Gln Trp Asn Val Asn Trp Glu Thr Arg Gln Val Val Ile Glu
 610 615 620

Phe Asp Gln Asn Val Phe Thr Ala Phe Thr Cys Leu Ser Ala Asp Cys
 625 630 635 640

Lys Ile Val His Glu Tyr Ile Gly Gly Tyr Ile Phe Leu Ser Thr Arg
 645 650 655

Ser Lys Asp Gln Asn Glu Thr Leu Asp Glu Asp Leu Phe His Lys Leu
 660 665 670

Thr Gly Gly Gln Asp
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<212> PRT

<213> Unknown

<220>

<223> Cytokine receptor extracellular motif found in many species.

<220>

<221> UNSURE

<222> (3)..(3)

<223> "Xaa" at position 3 can be any amino acid.

<400> 3

Trp Ser Xaa Trp Ser
 1 5

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